

AMENDMENTS TO THE CLAIMS

Please amend the claims as follows.

Please cancel claims 60, 78, 79, 84, 86, 88, 90, 92 to 94, 98, 101, 105, 149, 152, 164, 165 and 191, without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Claim 1 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising
(a) a nucleic acid sequence having at least 50% ~~[[85%]]~~ sequence identity to SEQ ID NO:29
~~SEQ ID NO:1~~ over a region of at least about 100 residues,

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region
of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region
of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region
of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region
of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a
region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a
region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a
region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a
region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a
region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

wherein the nucleic acid encodes a fluorescent polypeptide and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or

(b) a nucleic acid sequence completely complementary to (a).

Claims 2 to 13 (canceled)

Claim 14 (currently amended): The isolated, synthetic or recombinant nucleic acid of claim 1, wherein the fluorescent polypeptide comprises a green fluorescent protein.

Claim 15 (currently amended): The isolated, synthetic or recombinant nucleic acid of claim 1, wherein the fluorescent polypeptide comprises a cyan fluorescent protein.

Claims 16 to 28 (canceled)

Claim 29 (currently amended): An isolated, synthetic or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a sequence comprising

(a) a nucleic acid sequence as set forth in SEQ ID NO:29 ~~SEQ ID NO:1,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:3,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:5,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:7,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:9,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:11,~~

~~a nucleic acid sequence as set forth in SEQ ID NO:13,~~
~~a nucleic acid sequence as set forth in SEQ ID NO:15,~~
~~a nucleic acid sequence as set forth in SEQ ID NO:17,~~
~~a nucleic acid sequence as set forth in SEQ ID NO:19,~~
~~a nucleic acid sequence as set forth in SEQ ID NO:21,~~
~~a nucleic acid sequence as set forth in SEQ ID NO:23, or~~
~~a nucleic acid sequence as set forth in SEQ ID NO:25,~~

wherein the isolated, synthetic or recombinant nucleic acid encodes a fluorescent polypeptide, and the stringent conditions include a wash step comprising a wash in 0.2x SSC at a temperature of about 65°C for about 15 minutes; or

(b) a nucleic acid sequence completely complementary to (a).

Claims 30 to 32 (canceled)

Claim 33 (currently amended): A nucleic acid probe for identifying a nucleic acid encoding a fluorescent polypeptide, wherein the probe comprises at least 10 consecutive bases of a sequence comprising:

a sequence as set forth in SEQ ID NO:29 ~~SEQ ID NO:1,~~
~~a sequence as set forth in SEQ ID NO:3,~~
~~a sequence as set forth in SEQ ID NO:5,~~
~~a sequence as set forth in SEQ ID NO:7,~~
~~a sequence as set forth in SEQ ID NO:9,~~
~~a sequence as set forth in SEQ ID NO:11,~~
~~a sequence as set forth in SEQ ID NO:13,~~
~~a sequence as set forth in SEQ ID NO:15,~~
~~a sequence as set forth in SEQ ID NO:17,~~
~~a sequence as set forth in SEQ ID NO:19,~~
~~a sequence as set forth in SEQ ID NO:21,~~
~~a sequence as set forth in SEQ ID NO:23, or~~

~~a sequence as set forth in SEQ ID NO:25,~~

wherein the probe identifies the nucleic acid by binding or hybridization under stringent conditions, and the stringent conditions include a wash step comprising a wash in 0.2x SSC at a temperature of about 65°C for about 15 minutes; or

(b) a nucleic acid sequence completely complementary to (a).

Claim 34 (canceled)

Claim 35 (currently amended): A nucleic acid probe for identifying a nucleic acid encoding a fluorescent polypeptide, wherein the probe comprises a nucleic acid sequence of claim 1 or claim 29 comprising:

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

Claims 36 to 39 (canceled)

Claim 40 (currently amended): An amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of claim 1 or claim 29 as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 41 (canceled)

Claim 42 (currently amended): A method of amplifying a nucleic acid encoding a fluorescent polypeptide comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence comprising a sequence of claim 1 or claim 29 ~~as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 43 (currently amended): An expression cassette comprising a nucleic acid of claim 1 or claim 29 comprising

(i) ~~a nucleic acid comprising~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 44 (currently amended): A vector comprising a nucleic acid of claim 1 or claim 29 comprising

~~(i) a nucleic acid comprising~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,~~

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) ~~a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 45 (original): A cloning vehicle comprising a vector as set forth in claim 44, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

Claims 46 to 47 (canceled)

Claim 48 (currently amended): A transformed cell comprising a vector, wherein the vector comprises

[[~~(i)~~]] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or;~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID~~

~~NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 49 (currently amended): A transformed cell comprising

[[i)] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 50 (canceled)

Claim 51 (currently amended): A transgenic non-human animal comprising

[[(i)]] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID~~

~~NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof, or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claims 52 and 53 (canceled)

Claim 54 (currently amended): A transgenic plant comprising

[[~~(i)~~]] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 55 (canceled)

Claim 56 (currently amended): A transgenic seed comprising

[[~~(i)~~]] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a~~

~~subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claim 57 (canceled)

Claim 58 (currently amended): An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to

[[i)] a nucleic acid of claim 1 or claim 29 comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

Claims 59 to 86 (canceled)

Claim 87 (currently amended): An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 29.

Claims 88 to 105 (canceled)

Claim 106 (currently amended): A method for identifying a feature in a sequence comprising the steps of:

- (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a ~~polypeptide sequence and a nucleic acid sequence~~, wherein ~~the polypeptide comprises a polypeptide sequence as set forth in claim 60, and~~ the nucleic acid sequence comprises a sequence as set forth in claim 1 or claim 29.
- (b) identifying one or more features in the sequence with the computer program.

Claim 107 (currently amended): A method for comparing a first sequence to a second sequence comprising the steps of:

- (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a ~~polypeptide sequence or a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 or claim 29~~ or subsequence thereof; and
- (b) determining differences between the first sequence and the second sequence with the computer program.

Claims 108 to 110 (canceled)

Claim 111 (currently amended): A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

- (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable of amplifying a nucleic acid as set forth in claim 1 or claim 29 ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,~~

~~SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or a subsequence thereof;~~

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a fluorescent polypeptide from an environmental sample.

Claim 112 (canceled)

Claim 113 (currently amended): A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe as set forth in claim 33 or claim 35; comprising a sequence or a subsequence comprising:

~~(i) a nucleic acid comprising~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.~~

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample.

Claims 114 to 115 (canceled)

Claim 116 (currently amended): A method of generating a variant of a nucleic acid encoding a fluorescent protein comprising the steps of:

(a) providing a template nucleic acid comprising [(i)] a nucleic acid as set forth in claim 1 or claim 29; comprising

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof and~~

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

Claims 117 to 137 (canceled)

Claim 138 (currently amended): A method for modifying codons in a nucleic acid encoding a fluorescent polypeptide to increase its expression in a host cell, the method comprising

(a) providing a nucleic acid encoding a fluorescent polypeptide as set forth in claim 1 or claim 29; comprising a sequence selected from the group consisting of:

~~(i) a nucleic acid comprising~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues;~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues; or~~

~~a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues;~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof; and~~

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

Claims 139 to 142 (canceled)

Claim 143 (currently amended): A method for producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites or substrate binding sites, wherein the

modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence as set forth in claim 1 or claim 29 that ~~hybridizes under stringent conditions to a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO:1, a sequence as set forth in SEQ ID NO:3; a sequence as set forth in SEQ ID NO:5, a sequence as set forth in SEQ ID NO:7, a sequence as set forth in SEQ ID NO:9, a sequence as set forth in SEQ ID NO:11, a sequence as set forth in SEQ ID NO:13, and a sequence as set forth in SEQ ID NO:15 or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof, or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof, and the nucleic acid encodes a fluorescent polypeptide active site; [[and]]~~

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites.

Claim 144 to 173 (canceled)

Claim 174 (currently amended): A method for using a nucleic acid encoding a fluorescent polypeptide in gene therapy comprising the following steps:

- (a) obtaining from a patient a viable sample of primary cells of a particular cell type;
- (b) inserting in the cells of step (a) a nucleic acid segment encoding a desired gene product;
- (c) introducing in the cell of step (b) a vector comprising a nucleic acid as set forth in claim 1 or claim 29 of the invention;
- (d) identifying and isolating cells or cell lines that express the gene product of step (b);

- (e) re-introducing the cells that express the gene product;
- (f) removing from the patient an aliquot of tissue including cells resulting from step (d) and their progeny;
- (g) determining the quantity of the cells resulting from the step (d) in the aliquot of step (f), thereby the introduction of the vector of step (c) ~~comprising the nucleic acid of the invention~~ in addition to the desired gene allows the identification of viable cells that contain and express the desired gene of step b.

Claim 175 (currently amended): A method of gene therapy comprising the following steps:

- (a) providing a plurality of tissue cells;
- (b) providing a retroviral vector encoding a desired gene product;
- (c) providing a vector comprising a nucleic acid as set forth in claim 1 or claim 29 of the invention; and
- (d) contacting the target cells of step (a) with the retroviral vectors of step (b) and a vector of step (c) ~~the invention~~ under conditions wherein the cells of step (a) are transfected with the vectors of steps (b) and (c) allowing co-expression of the nucleic acid ~~polypeptide of the invention~~, thereby allowing assessment of proportion of transfected cells and levels of expression.

Claim 176 (canceled)

Claim 177 (currently amended): A method for diagnostic testing comprising the following steps:

- (a) providing a nucleic acid ~~vector of the invention~~ as set forth in claim 1 or claim 29 ~~[[44]]~~;
- (b) placing the nucleic acid ~~vector~~ of step (a) under control of a promoter;
- (c) providing an inducing agent to induce the promoter of step (b); and
- (d) contacting the agent of step (c) with the promoter of step (b) under condition wherein the agent of step (c) induces the promoter of step (b), thereby causing the expression of the nucleic acid and expression of a fluorescent polypeptide in cells, cell lines or tissues, wherein the cells, cell lines or tissue will become fluorescent in the presence of the inducing agent.

Claims 178 to 181 (canceled)

Claim 182 (currently amended): A method for assessing the effect of selected culture components and conditions on selected gene expression comprising the following steps:

(a) providing a cell comprising a nucleic acid as set forth in claim 1 or claim 29 operably linked to a regulatory sequence derived from a selected gene;

(b) incubating the cell of step (a) under selected culture conditions or in the presence of selected components, ~~thereby wherein~~ expressing a ~~[[the]]~~ polypeptide encoded by the nucleic acid of step (a) the invention; and

(c) detecting the presence and subcellular localization of fluorescent signal thereby assessing the effect of selected cultures components or condition on selected gene expression.

Claim 183 (canceled)

Claim 184 (currently amended): A method for assessing a mutagenic potential of a test agent in a tissue culture or transgenic animal comprising the following steps:

(a) providing a ~~[[the]]~~ nucleic acid ~~of the invention~~ as set forth in claim 1 or claim 29 operably linked to a transcriptional control element, wherein the transcription control element can be negatively regulated by a repressor;

(b) providing a repressor under control of a constitutively expressed gene;

(c) providing a test compound capable of interacting with a promoter of the constitutively expressed gene thereby turning it off; and

(d) contacting the test agent of step (c) with the repressor of step (b) under conditions wherein the test agent inactivates or turns off the gene expressing the repressor thereby causing the expression of the nucleic acid of step (a) polypeptide of the invention.

Claims 185 to 186 (canceled)

Claim 187 (currently amended): A method for identifying a compound capable of changing expression of a target gene comprising of the following steps:

(a) providing a first nucleic acid having a sequence as set forth in claim 1 or claim 29 and expressing a first polypeptide, wherein the nucleic acid is operably linked to a promoter of a target gene in a cell;

(b) providing a second nucleic acid as set forth in claim 1 or claim 29, and expressing a second polypeptide, wherein the second nucleic acid is operably linked to a promoter of a constitutively expressed gene in a cell, wherein the first polypeptide emits a light at a wavelength different than the wavelength of the light emitted by the second polypeptide;

(c) providing a compound affecting the expression of the target gene of step (a) by binding to the promoter of the target gene;

(d) contacting the compound of step (c) with the cell of step (a);

(e) expressing the first and second polypeptide, and

(f) detecting fluorescence of the first and second polypeptides,

(i) wherein altered fluorescence of the first polypeptide and unchanged fluorescence of the second polypeptide demonstrates that the compound binds to the target gene promoter and has no non-specific or cytotoxic effects thereby not altering expression of the second polypeptide; or

(ii) wherein altered fluorescence of the first polypeptide and altered fluorescence of the second polypeptide demonstrates that the test drug has non-specific or cytotoxic effects thereby affecting the expression of the second polypeptide.

Claim 188 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising a sequence encoding a fluorescent protein and having at least about 50%, ~~51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%~~ sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID

~~NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.~~

Claim 189 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising a sequence as set forth in ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135,~~

~~SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.~~

Claim 190 (currently amended): An isolated, synthetic or recombinant nucleic acid encoding a polypeptide comprising a sequence having at least about ~~50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%~~ sequence identity to ~~SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198.~~

Claim 191 (canceled)

Claim 192 (currently amended): An isolated, synthetic or recombinant nucleic acid encoding a fluorescent protein and having a sequence comprising any combination of segments whose overhangs as described in Figure 15 can anneal to each other.

Claim 193 (new): The isolated, synthetic or recombinant nucleic acid of claim 1, wherein the sequence identity to SEQ ID NO:29 is determined over a region of at least about 200 residues.

Claim 194 (new): The isolated, synthetic or recombinant nucleic acid of claim 193, wherein the sequence identity to SEQ ID NO:29 is determined over a region of at least about 300 residues.

Claim 195 (new): The isolated, synthetic or recombinant nucleic acid of claim 194, wherein the sequence identity to SEQ ID NO:29 is determined over a region of at least about 400 residues.

Claim 196 (new): The isolated, synthetic or recombinant nucleic acid of claim 195, wherein the sequence identity to SEQ ID NO:29 is determined over a region of at least about 500 residues.

Claim 197 (new): The isolated, synthetic or recombinant nucleic acid of claim 196, wherein the sequence identity to SEQ ID NO:29 is determined over a region of at least about 600 residues.

Claim 198 (new): The isolated, synthetic or recombinant nucleic acid of claim 1 or claim 188, wherein the nucleic acid sequence has at least 55% sequence identity to SEQ ID NO:29.

Claim 199 (new): The isolated, synthetic or recombinant nucleic acid of claim 198, wherein the nucleic acid sequence has at least 60% sequence identity to SEQ ID NO:29.

Claim 200 (new): The isolated, synthetic or recombinant nucleic acid of claim 199, wherein the nucleic acid sequence has at least 65% sequence identity to SEQ ID NO:29.

Claim 201 (new): The isolated, synthetic or recombinant nucleic acid of claim 200, wherein the nucleic acid sequence has at least 70% sequence identity to SEQ ID NO:29.

Claim 202 (new): The isolated, synthetic or recombinant nucleic acid of claim 201, wherein the nucleic acid sequence has at least 75% sequence identity to SEQ ID NO:29.

Claim 203 (new): The isolated, synthetic or recombinant nucleic acid of claim 202, wherein the nucleic acid sequence has at least 80% sequence identity to SEQ ID NO:29.

Claim 204 (new): The isolated, synthetic or recombinant nucleic acid of claim 203, wherein the nucleic acid sequence has at least 85% sequence identity to SEQ ID NO:29.

Claim 205 (new): The isolated, synthetic or recombinant nucleic acid of claim 204, wherein the nucleic acid sequence has at least 90% sequence identity to SEQ ID NO:29.

Claim 206 (new): The isolated, synthetic or recombinant nucleic acid of claim 205, wherein the nucleic acid sequence has at least 95% sequence identity to SEQ ID NO:29.

Claim 207 (new): The isolated, synthetic or recombinant nucleic acid of claim 206, wherein the nucleic acid sequence has at least 98% sequence identity to SEQ ID NO:29.

Claim 208 (new): The isolated, synthetic or recombinant nucleic acid of claim 207, wherein the nucleic acid sequence is SEQ ID NO:17.

Claim 209 (new): The isolated, synthetic or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence is SEQ ID NO:151, SEQ ID NO:193, SEQ ID NO:195 or SEQ ID NO:23.

Claim 210 (new): The isolated, synthetic or recombinant nucleic acid of claim 198, wherein the nucleic acid sequence is SEQ ID NO:147 or SEQ ID NO:7.

Claim 211 (new): The isolated, synthetic or recombinant nucleic acid of claim 199, wherein the nucleic acid sequence is SEQ ID NO:31, SEQ ID NO:159, SEQ ID NO:85, SEQ ID NO:111, SEQ ID NO:179 or SEQ ID NO:47.

Claim 212 (new): The isolated, synthetic or recombinant nucleic acid of claim 200, wherein the nucleic acid sequence is SEQ ID NO:71, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:49, SEQ ID NO:75, SEQ ID NO:163 or SEQ ID NO:97.

Claim 213 (new): The isolated, synthetic or recombinant nucleic acid of claim 201, wherein the nucleic acid sequence is SEQ ID NO:81, SEQ ID NO:35, SEQ ID NO:39, SEQ ID NO:57, SEQ ID NO:171, SEQ ID NO:27, SEQ ID NO:83 or SEQ ID NO:79.

Claim 214 (new): The isolated, synthetic or recombinant nucleic acid of claim 202, wherein the nucleic acid sequence is SEQ ID NO:101, SEQ ID NO:125, SEQ ID NO:87, SEQ ID NO:103, SEQ ID NO:135, SEQ ID NO:169, SEQ ID NO:119, SEQ ID NO:131, SEQ ID NO:167, SEQ ID NO:73, SEQ ID NO:109, SEQ ID NO:137, SEQ ID NO:127, SEQ ID NO:133, SEQ ID NO:139, SEQ ID NO:181, SEQ ID NO:89, SEQ ID NO:153, SEQ ID NO:69, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:59, SEQ ID NO:77, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:185, SEQ ID NO:143, SEQ ID NO:41, SEQ ID NO:121, SEQ ID NO:51, SEQ ID NO:37, SEQ ID NO:55, SEQ ID NO:43, SEQ ID NO:129, SEQ ID NO:99 or SEQ ID NO:141.

Claim 215 (new): The isolated, synthetic or recombinant nucleic acid of claim 203, wherein the nucleic acid sequence is SEQ ID NO:187, SEQ ID NO:123, SEQ ID NO:65, SEQ ID NO:93, SEQ ID NO:91, SEQ ID NO:189, SEQ ID NO:61, SEQ ID NO:95, SEQ ID NO:53, SEQ ID NO:145, SEQ ID NO:45, SEQ ID NO:165, SEQ ID NO:173, SEQ ID NO:177 or SEQ ID NO:161.

Claim 216 (new): The isolated, synthetic or recombinant nucleic acid of claim 204, wherein the nucleic acid sequence is SEQ ID NO:175, SEQ ID NO:157 or SEQ ID NO:149.

Claim 217 (new): A recombinant nucleic acid encoding a fluorescent protein made by a process comprising the following steps:

(a) providing a template nucleic acid comprising at least a sequence as set forth in claim 1;
and

(b) generating a recombinant nucleic acid encoding a fluorescent protein by subjecting the template nucleic acid to Synthetic Ligation Reassembly (SLR).

Claim 218 (new): The recombinant nucleic acid of claim 217, further comprising a step (e) expressing the assembled fluorescent protein-encoding nucleic acid of (d) to generate a fluorescent protein.

Claim 219 (new): The recombinant nucleic acid of claim 217, wherein the template nucleic acid comprises SEQ ID NO:29, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:23, SEQ ID NO:7 or SEQ ID NO:17.

Claim 220 (new): The recombinant nucleic acid of claim 217, further comprising at least a second template nucleic acid comprising SEQ ID NO:29, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:23, SEQ ID NO:7 or SEQ ID NO:17.

Claim 221 (new): A method for making a nucleic acid encoding a fluorescent protein comprising the following steps:

(a) providing a template nucleic acid comprising at least a sequence as set forth in claim 1;
and

(b) generating a recombinant nucleic acid encoding a fluorescent protein by subjecting the template nucleic acid to Synthetic Ligation Reassembly (SLR).

Claim 222 (new): The method of claim 221, further comprising a step (e) expressing the assembled fluorescent protein-encoding nucleic acid of (d) to generate a fluorescent protein.

Claim 223 (new): The method of claim 221, wherein the template nucleic acid comprises SEQ ID NO:29, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:23, SEQ ID NO:7 or SEQ ID NO:17.

Claim 224 (new): The method of claim 223, further comprising at least a second template nucleic acid comprising SEQ ID NO:29, SEQ ID NO:27, SEQ ID NO:31, SEQ ID NO:23, SEQ ID NO:7 or SEQ ID NO:17.

Claim 225 (new): A recombinant nucleic acid encoding a fluorescent protein codon-optimized for expression in a host cell, made by the process of claim 138.

Claim 226 (new): An isolated, synthetic or recombinant nucleic acid encoding a fluorescent protein comprising a sequence as set forth in claim 1, and further comprising codons optimized for expression in a host cell.

Claim 227 (new): An isolated, synthetic or recombinant nucleic acid encoding a fluorescent protein comprising a sequence as set forth in claim 1, and further comprising coding sequence for a tag or a reporter sequence, and optionally the tag or reporter sequence comprises an epitope tag, a fluorescent tag, a genetic reporter or a protein tag.

Claim 228 (new): The nucleic acid probe of claim 35, further comprising an epitope tag or a fluorescent tag.